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	A3	Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science vol.247:1306-1310 (Mar. 1990).	
	A4	Bowie, J.U., et al., "A Method to Identify Protein Sequences that Fold into a Known Three-Dimensional Structure", Science vol.253:164-170 (Jul. 1991).	
	A5	Brooks et al., "CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations," J. of Computational Chemistry, 4(2):187-217 (1983).	
	A6	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science vol.221(4612):709-713 (Aug. 1983).	
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	A8	Dahiyat, B.I., et al., "Automated design of the surface positions of protein helices", Protein Science 6:1333-1337 (Jun. 1997).	
	A9	Dahiyat et al., "Protein design automation," Caltech Biology Annual Report, 172 (1995).	
	A10	Dahiyat, B.I., et al., "Proteins from Scratch", press digest email by Science (Sep. 26, 1997).	
	A11	Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science vol. 4, Suppl. 2, 83 (1995).	
	A12	Dahiyat et al., "Protein design Automation," Poster Sessions, Protein Science vol.5, Suppl. 1, 22-23 (1996).	
	A13	Dahiyat et al., "De Novo Protein Design: Fully Automated Sequence Selection," Science, 278:82-87 (1997).	
	A14	Dahiyat et al., "Probing the Role of Specificity in Protein Design," Caltech Biology Annual Report, 160-161 (1996).	
	A15	Dahiyat et al., "Protein Design Automation," 1996, Protein Science, vol. 5, pp. 895-903, Nov. 30, 1999.	
	A16	Dahiyat, B.I., et al., "First fully automatic design of a protein achieved by Caltech scientists", new press release (Oct. 1997).	
	A17	Dalal, S., et al., "Protein alchemy: Changing .beta.-sheet into .alpha.-helix", Nature Struc. Biol. vol.4(7):548-552 (Jul. 1997).	

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Application Number	09/837,886				
Filing Date	April 18, 2001				
First Named Inventor	MAYO, Stephen L.				
Group Art Unit	1636				
Examiner Name	TECH CENTER 1600/2900				
Sheet	2	of	4	Attorney Docket Number	A-65353-8/RFT/RMS/RMK

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	B5	Desmet, J., et al., "The dead-end elimination theorem and its use in protein side-chain positioning", Nature vol.356:539-542 (Apr. 1992).	
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	B8	Eisenberg, D., et al., "Solvation energy in protein folding and binding", Nature vol.319:199-203 (Jan. 1986).	
	B9	Goldstein, R.F., "Efficient Rotamer Elimination Applied to Protein Side-Chains and Related Spin Glasses", Biophys. Jour. vol.66:1335-1340 (May 1994).	
	B10	Gordon et al. "Energy functions for protein design," Curr. Opinion in Struct. Biol., 9:509-513 (1999).	
	B11	Harbury et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils," Proc. Natl. Acad. Sci. USA, 92:8408-8412 (1995).	
	B12	Harbury et al., "High-Resolution Protein Design with Backbone Freedom," Science, 282:1462-1467 (1998).	
	B13	Hellinga, H.W., et al., "Construction of New Ligand Binding Site in Proteins of Known Structure", J. Mol. Biol. 222:763-785 (1991).	
	B14	Hellinga, H.W., "Rational protein design: Combining theory and experiment", Proc. Natl. Acad. Sci. USA vol.94:10015-10017 (Sep. 1997).	
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	B16	Holmes, "First-ever designer protein fits like a glove," New Scientist, IPC Magazines Limited, Oct. 11, 1997 (1997).	
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	C2	Koehl et al., "De Novo Protein Design. I. In Search of Stability and Specificity," J. Mol. Biol., 293:1161-1181 (1999).	
	C3	Kono et al., "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation Prediction from Given Backbone Geometry," Proteins: Structure, Function, and Genetics, 19:244-255 (1994).	
	C4	Kortemme et al., "Design of a 20-Amino Acid, Three-Stranded β -Sheet Protein," Science, 281:253-256 (1988).	
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	C7	Lazar et al., "De novo design of the hydrophobic core of ubiquitin," Protein Science 6:1167-1178 (1997).	
	C8	Lee et al., "Accurate prediction of the stability and activity effects of site-directed mutagenesis on a protein core," Nature, 352:448-451 (1991).	
	C9	Lim et al., "The crystal structure of a mutant protein with altered but improved hydrophobic core packing," Proc Natl Acad Sci U S A. 1994 Jan 4;91(1):423-7	
	C10	Mayo et al., "DREIDING: A Generic Force Field for Molecular Simulations," J. Phys. Chem., 94:8897-8909 (1990).	
	C11	Minor Jr., D.L., "Measurement of the β -sheet-forming propensities of amino acids", Nature vol.367:660-663 (Feb. 1994).	
	C12	Munoz, V., et al., "Helix design, prediction and stability", Curr. Opin. in Biotech. 6:382-386 (Aug. 1995).	
	C12	Munoz, V., et al., "Intrinsic Secondary Structure Propensities of the Amino Acids, Using Statistical phi-psi Matrices: Comparison with Experimental Scales", Proteins 20:301-311 (1994).	
	C14	Munoz, V., et al., "Analysis of the effect of local interactions on protein stability", Folding & Design 1(3):167-178 (Apr. 1996).	
	C15	Pabo, C., "Designing proteins and peptides", Nature vol.301:200 (Jan. 1983).	
	C16	Padmanabhan, S., et al., "Relative helix-forming tendencies of nonpolar amino acids", Nature vol.344:268-270 (Mar. 1990).	
	C17	Ponder, J.W., et al., "Use of Packing Criteria in the Enumeration of Allowed Sequences for Different Structural Classes", release by Acad. Press Inc. (London) Ltd. pp.775-791(1987).	
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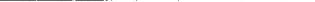
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	D1	Regan, L., "Helix is a helix is a helix?", Proc. Natl. Acad. Sci. USA vol.94:2796-2797 (Apr. 1997).
	D2	Smith, C.K., et al., "Guidelines for Protein Design: The Energetics of .beta. Sheet Side Chain Interactions", Science vol.270:980-982 (Nov. 1995).
	D3	Stickle et al., "Hydrogen Bonding in Globular Proteins," (1992) Journal of Molecular Biology, vol.226, pp. 1143-1159.
	D4	Sun, S., et al., "Designing amino acid sequences to fold with good hydrophobic cores", Protein Eng. vol.8(12):1205-1213 (1995).
	D5	Tuffery et al., "A New Approach to the Rapid Determination of Protein Side Chain Conformations," J. of Biomolecular Struct. & Dynamics, 8(6):1267-1289 (1991).
	D6	van Gunsteren et al., "Prediction of the Activity and Stability Effects of Site-directed Mutagenesis on a Protein Core," J. Mol. Biol., 227:389-395 (1992).
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	D9	Wodak, S.J., et al., "Analytical approximation to the accessible surface area of proteins", Proc. Natl. Acad. Sci. USA vol.77(4):1736-1740 (Apr. 1980).

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